



60

```

GTCCTTCCACCATGCACTCGCTGGGTTCTCTGTGGGTCTCTGCTCGCCGCTG
-----+-----+-----+-----+-----+-----+-----+
CAGGAAGGGTGTACGTGAGCGACCGAAGAAGACACCGCACAAAGAGACGAGGGCGAC
M H S L G F F S V A C S L L A A A

```

1

CGCTGGTCCCCGGGTCTCGGAGGGCCCGGCCGCGCCGCTTCGAGTCGGACTCG
 - - + - - + - - + - - + - - + - - + - - + - - + - - +
 GCGACGGGCCAGGGAGCGCTCCGGGGGGGGGGGGGGAAAGCTCAGGCCTGAGC
 L L P G P R E A P A A A A F E S G L D

61

ACCCTCTGGACGCGGGAGCCCCGACGGGGCGAGGGCCACGGCTTATGCAAAGATACTGG
 TGGAGAGCCTTGCGGCCCTGGGTGCGCCCGCTCCGGTGGCGAATAACGTTCGTTCTAGACC
 L S D A E P D A G E A T A Y A S K D L E

121

18

ATTGGAAAATGTACAAGTGTCAAGCTAAGGAAAGGGGGCTGGCAACATAACAGAGAACAGG
 TAAACCTTTACATGTTCACAGTCGATTCCCTGCACCGTTGTATTGTCCTTGTC
 W K M Y K C O L R K G G W Q H N R E Q A

241

CCAACCTCAACTCAAGGACAGAAAGAGACTATAAAATTGGCTGCAGCACATTATAATACAG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GGTGGAGTTGAGTTCTGTCTCTGATATTAAACGACGTCGTGAATTATTATGTC
N L N S B T E E T I K F A A H Y N T E

103

FIG. 1A MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

361 AGATCTTGAAAGTATTGATAATGAGTGGAGAAAAGACTCAATGCATGCCACGGAGGTGT
TCTAGAACTTTCATAACTATTACTCACCTCTTGAGTTACGTACGGTGCCTCCACA
I L K S I D N E W R K T Q C M P R E V C
GTATAGATGTGGGAAGGAGTTGGAGTCGGACAAACACCTTCTTTAACCTCCATGTG
CATATCTACACCCCTTCTCAAACCTCAGCGCTGTTGTGGAAAGAAATTGGAGGTACAC
I D V G K E F G V A T N T F F K P P C V
TGTCGGTCTACAGATGTGGGGTTGCTGCAAATAGTGGAGGGCTGCAGTGCATGAAACACCA
ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT
S V Y R C G G C C N S E G L Q C M N T S
GCACGGCTACTCTAGCAAAGACGTTATTGAAATTACAGTGCCTCTCTCAAGGCCCA
CGTGCTCGATGGAGTCGTTCTGCAAATAAACCTTAATGTCACGGAGAGAGTTCCGGGGT
T S Y L S K T L F E I T V P L S Q G P K
AACCAGTAACATCAGTTGGCAAATCACACTTCCCGATGCATGTCATAACTGGATG
TTGGTCATTGTAGTCAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC
P V T I S F A N H T S C R C M S K L D V

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MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

O I P E
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| | | |
|-----|--|-----|
| 661 | TTTACAGACAAGTTCATCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
AAATGTCTGTTCAAGTAAGGTAAATAATCTGCAAGGGACGGTGTGATGGTGTCAAG
Y R Q V H S I I R R S L P A T L P Q C Q | 720 |
| 721 | AGGCAGCGAACAGACCTGCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
TCCGTCGCTTGTTCTGGACGGGGGGTTAATGTACACCTTATTAGTGTAGACGTCAGGG
A A N K T C P T N Y M W N N H I C R C L | 780 |
| 781 | TGGCTCAGGAAGATTATGTTTCCTCGGATGCTGGAGATGGACTCAACAGATGGATTCC
ACCGAGTCCTCTAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
A Q E D F M F S S D A G D S T D G F H | 840 |
| 841 | ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTTGTCTGCAGAG
TACTGTAGACACCTGGTTGTTCTCGACCTACTTCTGGACAGTCACACAGACGTCTC
D I C G P N K E L D E E T C Q C V C R A | 900 |
| 901 | CGGGCTTCGGCCTGCCAGCTGTGGACCCACAAAGAACTAGACAGAACTCATGCCAGT
GCCCGAAGCCGGACGGTCGACACCTGGGGTGTCTTGATCTGTCTTGTAGTACGGTCA
G L R P A S C G P H K E L D R N S C Q C | 960 |

FIG. 1C
MATCH WITH FIG. 1D

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U.S. GOVERNMENT

MATCH WITH FIG. 1C

GTGCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGCCAACCGAGAATTGTGATGAAA
961
-----+-----+-----+-----+-----+-----+-----+-----+
CACAGACATTGTGGTTGAGAAGGGGTGGTTACACCCCGGTTGGCTCTTAAACTACTTT
V C K N K L F P S Q C G A N R E F D E N

ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCAAGAAATTCAACCCCTAAATCCTGGAA
1021
-----+-----+-----+-----+-----+-----+-----+-----+
TGTGTACGGTCACACATACATTCTGGACGGGGTCTTTAGTTGGGATTAGGACCTT
T C Q C V C K R T C P R N Q P L N P G K

AATGTCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAAGGAAAGAAGTCC
1081
-----+-----+-----+-----+-----+-----+-----+-----+
TTACACGGACACTTACATGTCTTCAGGTGTCTTACGAACAATTTCCTTCTCAAGG
C A C E C T E S P Q K C L L K G K F H

ACCACCAAACATGCAGCTTACAGACGGCCATGTACGAACGCCAGAAGGCTTGTGAGC
1141
-----+-----+-----+-----+-----+-----+-----+-----+
TGGTGGTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCGAAACACTCG
H Q T C S C Y R R P C T N R Q K A C E P

CAGGATTTCATATACTGAAAGAAGTGTGTGTCATATTGGCAAAGACCAC
1201
-----+-----+-----+-----+-----+-----+-----+-----+
GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAAGTATAACCCGTTCTGGTG
G F S Y S E E V C R C V P S Y W Q R P Q

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MATCH WITH FIG. 1E

FIG. 1D



MATCH WITH FIG. 1D

| | | | |
|--|---|---|------|
| AAATGAGCTAAGATTGTACTGTTTCAGTTCATCGATTCTATTATGGAAAATCTGTT | M | * | 1320 |
| TACTCGATTCTAACATGACAAAGGTCAAGTAGCTAAAGATAATAACCTTTGACACA | M | S | |
| TGCCACAGTAGAACTGCTGTGAACAGAGAACCCCTGTGGGCCATGCTAACAAAGACA | | | 1321 |
| ACGGTGTCACTCTTGACAGACACTTGTCTCTGGAACACCCCAGTACGATTGTTCTGT | | | |
| AAAGTCTGTCTTCCCTGAACCAGTGGATAACTTACAGAAATGGACTGGAGCTCATCTG | | | 1380 |
| TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTACCTGACCTGAGTAGAC | | | |
| CAAAGGCCCTCTTGTAAAGACTGGTTCTGCCAATGACCAAAACGCCAAGATTTCCTC | | | 1440 |
| GTTTCCGGAGAACATTCTGACCAAAAGACGGTTACTGGTTGTGGTTCTAAAGGAG | | | |
| TTGTGATTCTTAAAGAATGACTATATAATTATTCCACTAAAAAATATTGTTCTGC | | | 1441 |
| AACACTAAAGAAATTCTTACTGATATAAAAGGTGATTTTATAACAAAGACG | | | |
| ATTCATTTTATAGCAACAAATTGGTAAACACTCACTGTGATCAATTATTTATATCAT | | | 1501 |
| TAAGTAAAATATCGTGTGTTAACCAATTGTGAGTGACACTAGTTATAAAATATAGTA | | | |
| GCAAAATATGTTAAAATGAAAATTGTATTATAAAAAAAAAAAAAAA | | | 1561 |
| CGTTTATACAAATTTTATTTTACTTTAACATAAAATTTTTTTTTTTTTTTTTT | | | |
| | | | 1620 |
| | | | 1674 |

EIGER



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| | | |
|-----|---|--|
| 1 | | CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGACAGTTACGGTCTGTGTCAGTGT |
| 61 | | AGATGAACTCATGACTCTACCCAGAATAATTGGAAAATGTACAAGTGTCTAGCTAACGAC |
| | M T V L Y P E Y W K M Y K C Q L R | +-----+-----+-----+-----+-----+-----+-----+ |
| 121 | | GAAAGGGCTGGCAACATAACAGAGAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAGAC |
| | K G G W Q H N R E Q A N L N S R T E E T | +-----+-----+-----+-----+-----+-----+-----+ |
| 181 | | TATAAAATTGCTGCAGCACATTATAACAGAGATCTGAAAGTTATGATAATGAGTG |
| | I K F A A H Y N T E I L K S I D N E W | +-----+-----+-----+-----+-----+-----+-----+ |
| 241 | | GAGAAAGACTCAAATGCATGCCACGGAGGTGTATAGATGTGGGAAGGGAGTTGGAGT |
| | R K T Q C M P R E V C I D V G K E F G V | +-----+-----+-----+-----+-----+-----+-----+ |
| 301 | | CGCGACAAACACCTTCTTAAACCTCCATGTTGTCAGATGTCGGTTGGCTG |
| | A T N T F E K D B C V S V V B C G C C C | +-----+-----+-----+-----+-----+-----+-----+ |

MATCH WITH FIG. 2B

FIG 2A

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PTAB

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MATCH WITH FIG. 2A

| | | |
|---|--|--|
| 421 | TGAAATTACAGTGCCTCTCTCAAGGCCAAACCAAGTAACAATCAGTTTGGCCAATCA | •
•
•
+-----+-----+-----+-----+-----+-----+-----+-----+ |
| E I T V P L S Q G P K P V T I S F A N H | | |
| 481 | CACTTCCTGCCGGATGCATGTCTAAACTGGATGTTACAGACAAGTCATTCCATTATTAG | •
•
•
+-----+-----+-----+-----+-----+-----+-----+-----+ |
| T S C R C M S K L D V Y R Q V H S I I R | | |
| 541 | ACGTTCCCTGCCAGAACACTACACAGTGTCAAGCGAACAAAGACCTGCCACCAA | •
•
•
+-----+-----+-----+-----+-----+-----+-----+-----+ |
| R S L P A T L P Q C Q A A N K T C P T N | | |
| 601 | TTACATGTGGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTATGTTTTCCTC | •
•
•
+-----+-----+-----+-----+-----+-----+-----+-----+ |
| Y M W N N H I C R C L A Q E D F M F S S | | |
| 661 | GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAAACAGGAGCT | •
•
•
+-----+-----+-----+-----+-----+-----+-----+-----+ |
| D A G D D S T D G F H D I C G P N K E L | | |
| 721 | GGATGAAAGAGACCTGTCAGTGTGCTGCAGAGGGGCTTCGGCCTGCCAGCTGTGGACC | •
•
•
+-----+-----+-----+-----+-----+-----+-----+-----+ |
| D E E T C Q C V C R A G L R P A S C G P | | |

FIG. 2B

MATCH WITH FIG. 2C

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MATCH WITH FIG. 2B

| | |
|------|--|
| 781 | CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCAGTGTAAACAAACTCTCCCCAG
H K E L D R N S C Q C V C K N K L F P S |
| 841 | CCAATGTGGGCCAACCGAGAATTGATGAAAACACATGCCAGTGTGATGTAAAGAAC
Q C G A N R E F D E N T C Q C V C K R T |
| 901 | CTGGCCCCAGAAATCAACCCCTAAATCCTGGAAAAATGTGCCTGTGAATGTACAGAAAGTCC
C P R N Q P L N P G K C A C E C T E S P |
| 961 | ACAGAAATGCTTGTGTTAAAGGAAAGTTCACACCACAAACATGCAGCTGTACAGACG
Q K C L L K G K F H H Q T C S C Y R R |
| 1021 | GCCATGTACCGAACCGGCCAGAAGGCTTGTGAGGCCAGGATTTCATATACTGAAAGAAGTGTG
P C T N R Q K A C E P G F S Y S E E V C |
| 1081 | TGTTGTGTCCTCATATTGGCAAAGAACCAAAATGAGCTAAGATTGACTGTTTCCA
R C V P S Y W Q R P Q M S * |

MATCH WITH FIG. 2D

FIG. 2C



MATCH WITH FIG. 2C

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FIG. 2D



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1 Pdgfa MRTILACLLL LGCCYLAWL AEEAEIPREV IERLARSQIH SIRDLORLLE
 Pdgfb MNRCWA. LFL SLCCYLRLLS AEGDPIPEEL YEMLSOHSIR SFDDLQRLLH
 Vegf MNFLL SWHAWSLALL LY LHHAKWSQA
 Vegf2 MTV LYPEYWKMVK CQ LRKGCGWQHN

50
 51 Pdgfa IDSVGSEDSL DTSRRAHGCVH ATKHIVPEKRP LPIRRKRSI EEAVP
 Pdgfb GDP.GEEDGA ELDLNMTRSH SGGELES LARGRRSLG SLTIAEPAMI
 Vegf APMAE GGCQ NHHEVVKFMD VYQR
 Vegf2 REQANLNNSRT EETIKFAAAH YNTEILKSID NEWRK

100

101 Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVWKQDPS
 Pdgfb AECKTRTEVF EISRRLIDRT NANFLWPPC VEVQRCGGCC NNRNVQCRPT
 Vegf SYCHPIETLY DIFQEYPDE ! . EYIFKPSV VPLMRCGGCC NDECLEQVPT
 Vegf2 TQGMPREVC1 DVGKEFGVAT . NTFKKPPC VSVYRCGGCC NSEGLQMN

150

151 Pdgfa RVHHRSWKVA KVEYVRKKPK LKEVQVRLEE HLEOAC AT
 Pdgfb QVQLRPVQVR KIEIVRKKPK FKKATVTLED HLACKC ETVAARPV
 Vegf EESNITMQIM RIK.PH.QC QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
 Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCROMSKL DVYRQVHSII

200

FIG. 3A



250

Pdgf^a TSLNPD YREEDTIVR
Pdgf^b RSPGGSQEQR AKTPQTIVTI RTVYVRRPK GKHRKFKHTH DKTALKETLGC
Vegf RGK GKGQKRK KSRYKSWSY VGARCCCLMPW SLPGPHP
Vegf² RRSUPATLPO CQAANKTCPT NYMMNNHICR CLAQEDFMFS SDAGDDSTDG

300

Pdgf^a
Pdgf^b A
Vegf CGP
Vegf² FHDICGPNE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCCQCVCNK

350

Pdgf^a
Pdgf^b
Vegf DSRCKARQ LEIERNTRCR DKPRR
Vegf² LFPSOCCGANR EFIDENTCQC VCKRTCPRNQ PLNFGKCAE CTESPQKCLL

398

Pdgf^a
Pdgf^b
Vegf
Vegf² KGKKFHHTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPMWS

FIG. 3B



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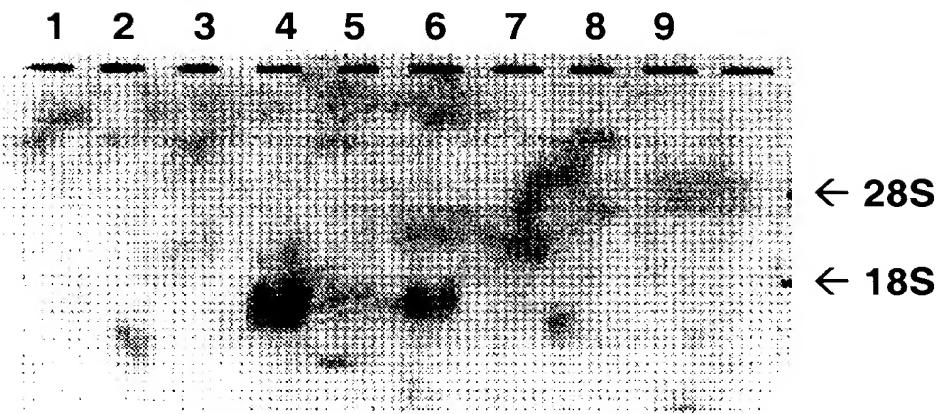
**PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN
EACH PAIR OF GENES IS SHOWN IN THE
FOLLOWING TABLE**

| | PDGF α | PDGF β | VEGF | VEGF-2 |
|---------------|---------------|--------------|------|--------|
| PDGF α | | | | |
| PDGF β | 48.0 | | | |
| VEGF | 20.7 | 22.7 | | |
| VEGF-2 | 28.5 | 22.4 | 30.0 | |

FIG. 4



Expression of VEGF2 mRNA in Human Breast Tumor Cells



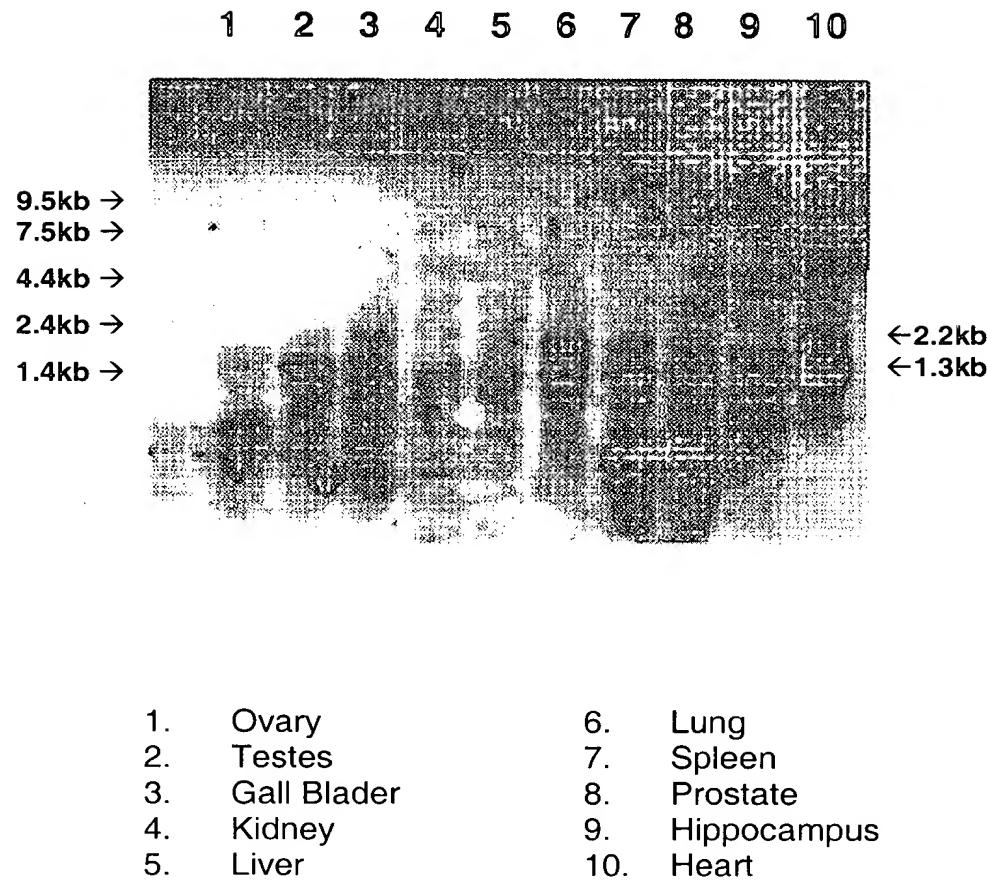
| | |
|-----------|-------------------------|
| Lane 1 | Normal Tissue |
| Lane 2 | Breast Tumor Tissue |
| Lanes 3-9 | Breast Tumor Cell Lines |

FIG. 5



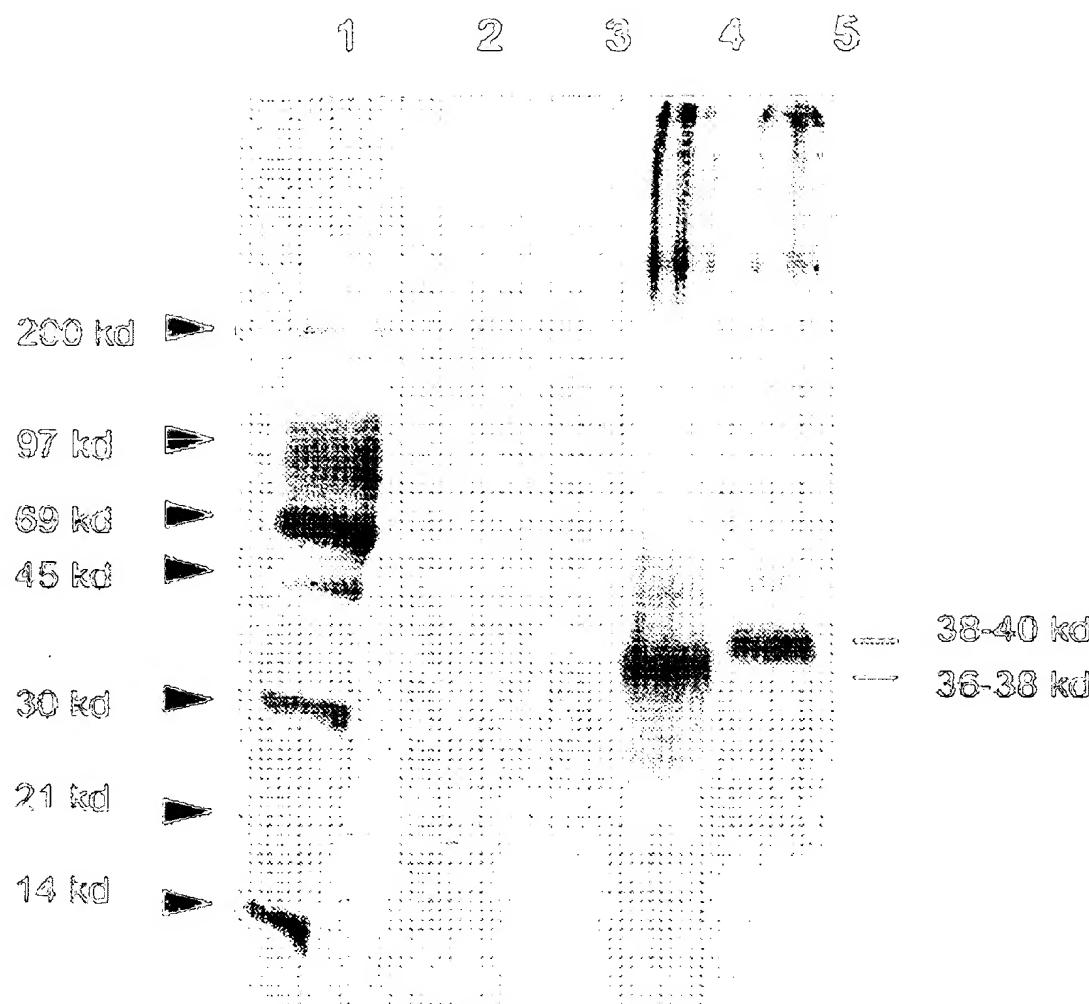
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Expression of VEGF2 mRNA in Human Adult Tissues



| | |
|----------------|----------------|
| 1. Ovary | 6. Lung |
| 2. Testes | 7. Spleen |
| 3. Gall Blader | 8. Prostate |
| 4. Kidney | 9. Hippocampus |
| 5. Liver | 10. Heart |

FIG. 6



Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse & forward primer)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primer)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primer)

FIG. 7

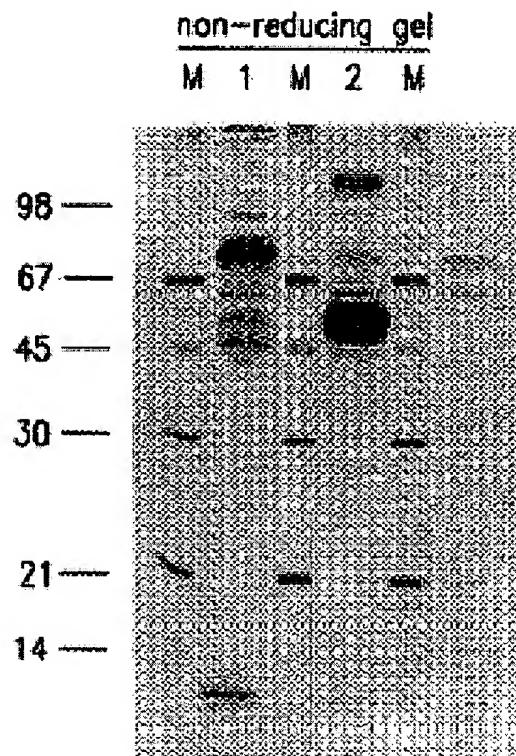
O P E SCITA
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RECEIVED

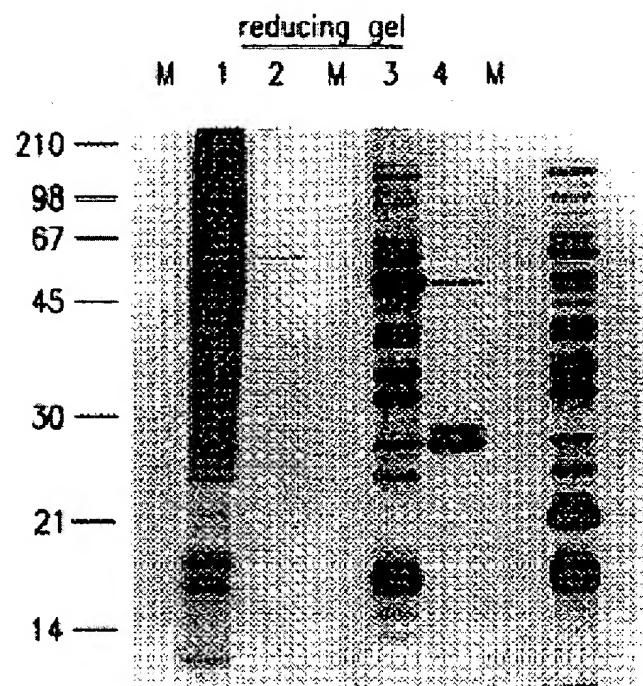
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Lane M: Marker
Lane 1: Vector medium
Lane 2: VEGF2 medium

FIG. 8A



Lane M: Marker
Lane 1: vector cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 cytoplasm
Lane 4: VEGF2 medium

FIG. 8B

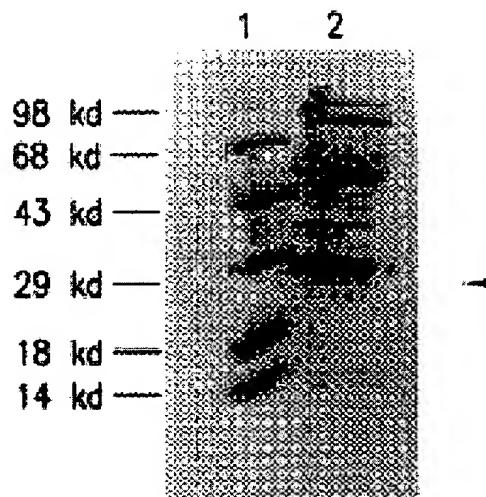


FIG. 9

Lane 1: Molecular weight marker
Lane 2: Precipitates containing VEGF2.

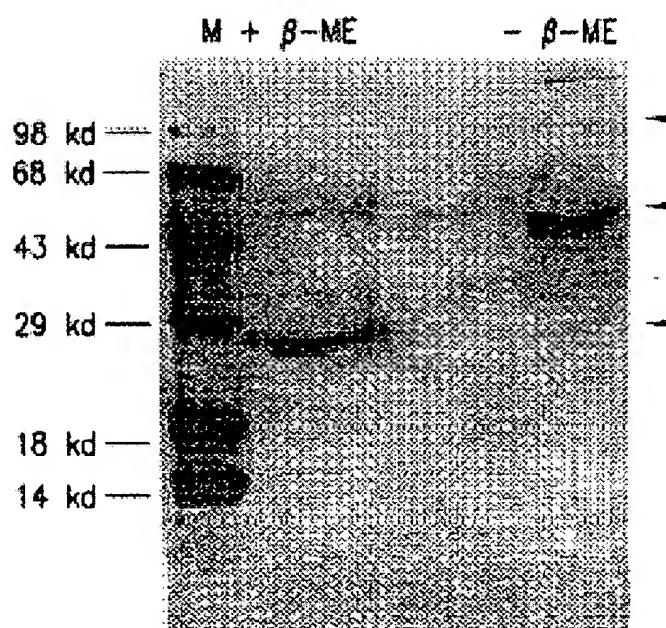


FIG. 10



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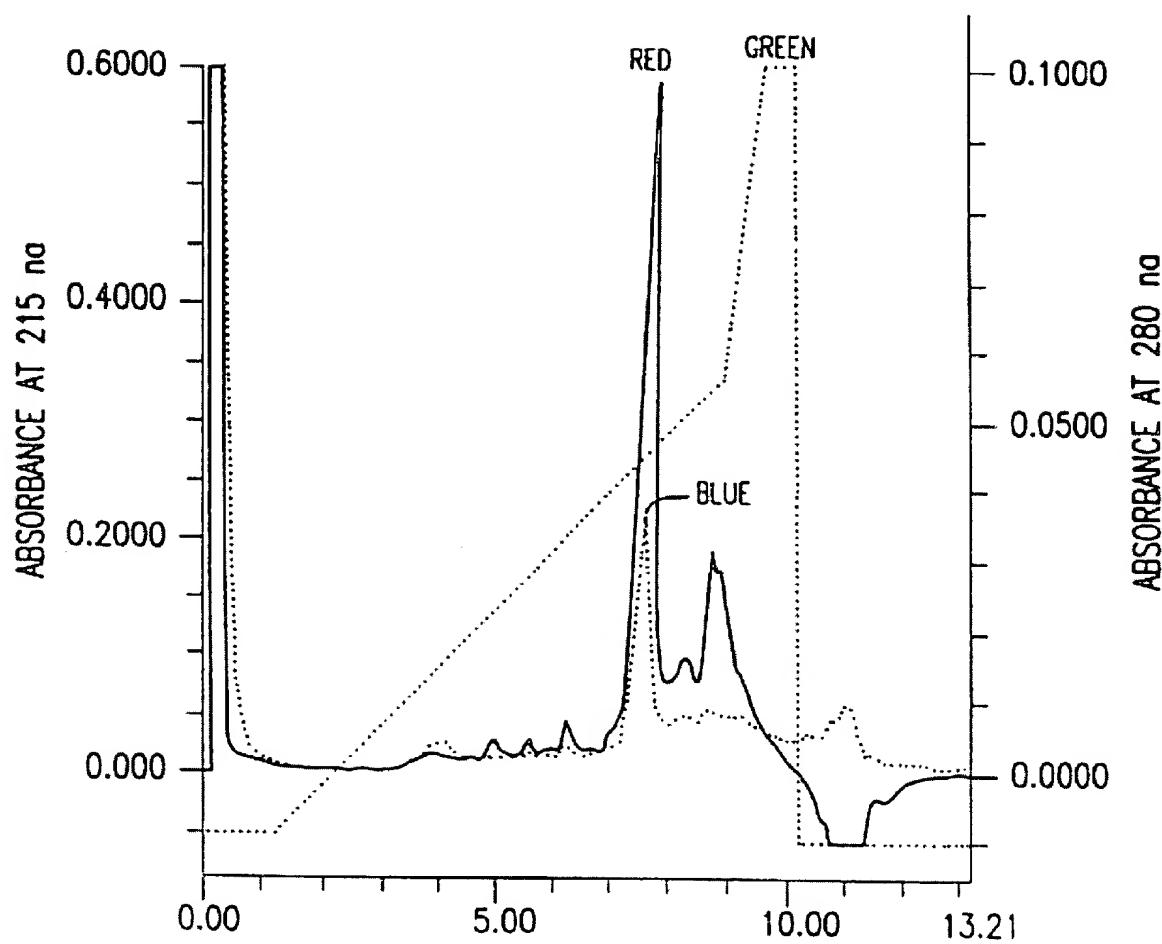


FIG. 11



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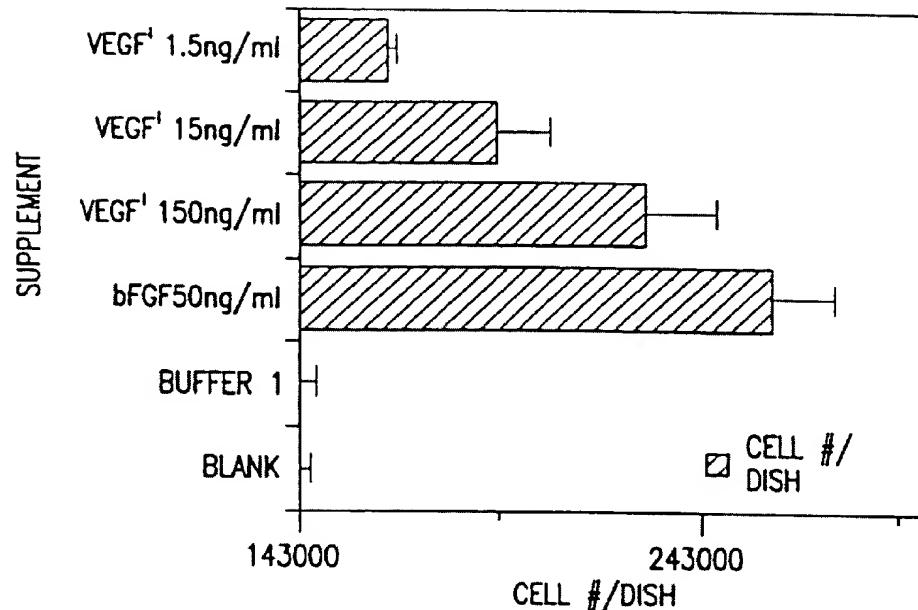


FIG. 12

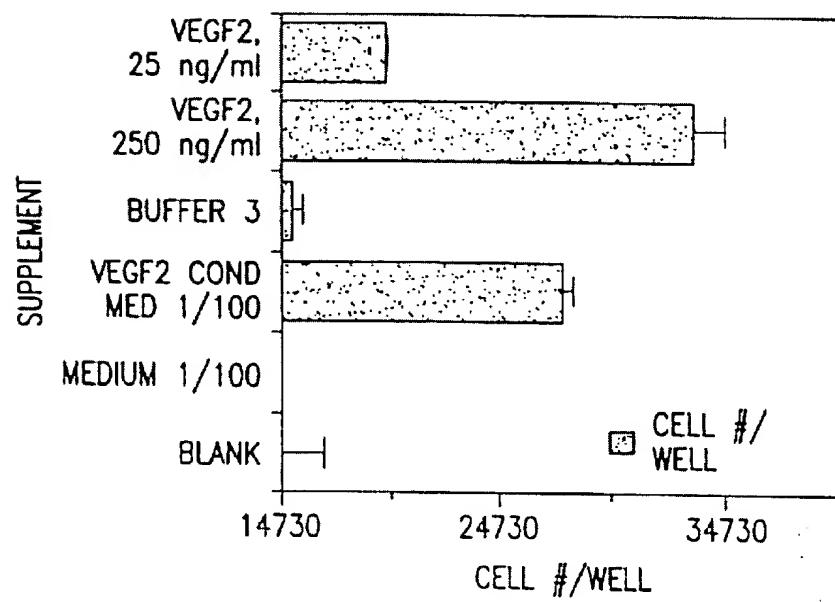


FIG. 13